

1/30

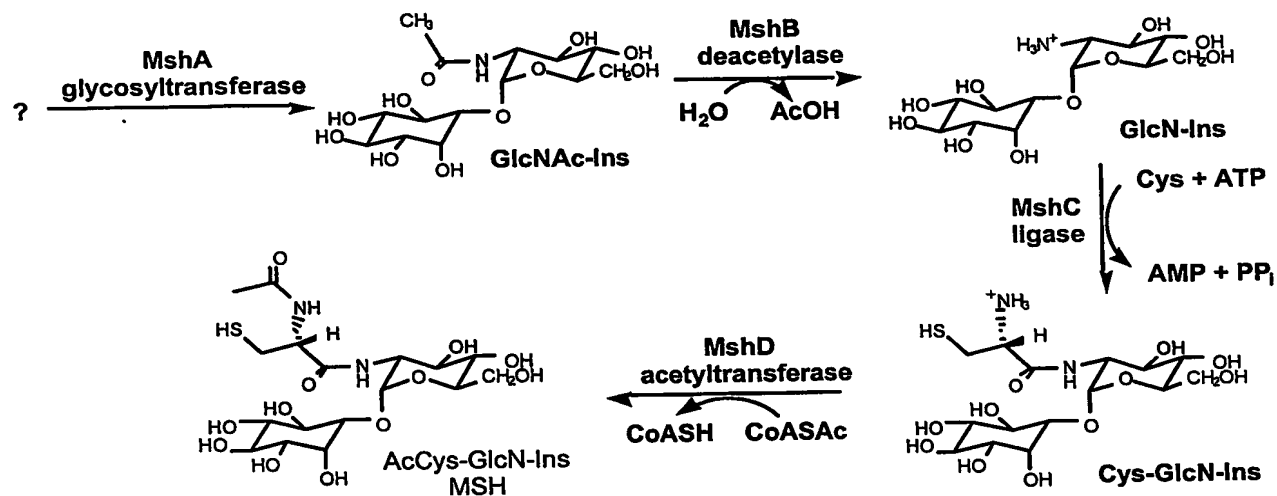


Figure 1

MshC nucleic acid sequence of *M. smegmatis*

ATGCAATCGTGGTCGGCACCGGCGATTCCGGTGGTTCCGGGACGTGGCCCTGCGCTG
CGCCTCTTCGACAGCGCTGATCGCCAGGTCCGGCCCGTCACACCGGGACCGACCGC
AACCATGTACGTGTGCGGCATCACCCATACGACGCGACCCATCTGGGTACGCCGC
GACCTATCTGACGTTTCGACCTGGTGCATCGCCTATGGCTCGACGCCGGACACACCGT
GCAGTACGTCCAGAACGTCACCGACGTGGACGACCCGTTGTTTCGAGCGTGCTGAGC
GCGACGGCATCGACTGGCGGACGCTGGGCGACCGCGAGACGCAGCTGTTCCGTGAG
GACATGGCCGCGTTGCGCGTGCTGCCCCGCACGACTACGTCGCCGCGACCGACGC
GATCGCCGAGGTCGTCGAGATGGTCGAGAAGCTGCTGGCCTCGGGTGCGGCGTACA
TCGTCGAGGACGCCGAGTACCCCGACGTGTACTTCCGCGCCGACGCCACCGCGCAG
TTCGGGTACGAGTCCGGCTACGACCGCGACACCATGCTCACGTTGTTTCGCCGAACGC
GGCGGGGACCCGGACCGCCCGGGCAAGTCCGATCAACTCGACGCGTTGCTGTGGCG
CGCCGAGCGTCCTGGCGAGCCAGCTGGCCTTCGCCGTTTCGGCCGGGGCCGGCCCCG
GCTGGCACGTGGAATGTTTCGGCGATCGCCCTGACGCGGATCGGCACCGGCCTCGAC
ATCCAGGGCGGGCGGCAGCGACCTCATCTTCCCGCACACGAGTATTCGGCCGCGCA
CGCCGAATCCGTCACCGGTGAGCGACGATTCGCACGCCACTACGTGCACACCGGCA
TGATCGGCTGGGACGGCCACAAGATGAGCAAGAGCCGCGGCAACCTGGTCCTGGTG
TCGCAGTTGCGCGCCCAGGGCGTCGACCCGTCGGCGATCCGGCTCGGCCTGTTCTCC
GGGCACTACCGCGAGGACCGGTTCTGGAGCAACGAGGTTCTCGACGAGGCCAACGC
GCGACTCGCGCGGTGGCGCAGTGCCACCGCATTGCCCGAGGCGCCCGATGCGACCG
ACGTGATCGCGCGCGTCCGGCAGTACCTGGCCGATGACCTGGACACGCCGAAAGCG
CTTGCCGCACTCGATGGTTGGTGTACCGACGCGCTGTCCTACGGTGGGCACGACACC
GAGTCGCCGCGGCTCGTGGCCACCACCGTCGACGCGTTGCTGGGTGTGGACCTC

Figure 2A

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MshC amino acid sequence of *M. smegmatis* (PMshCMs)

MQSWSAPAIP VVPGRGPALR LFDSADRQVR PVTPGPTATM
YVCGITPYDA THLGHAATYL TFDLVHRLWL DAGHTVQYVQ
NVTDVDDPLF ERAERDGDW RTLGDRETQL FREDMAALRV
LPPHDYVAAT DAIAEVVEMV EKLLASGAAY IVEDAEYPDV
YFRADATAQF GYESGYDRDT MLTLFAERGG DPDRPGKSDQ
LDALLWRAER PGEPSWPSPF GRGRPGWHVE CSAIALTRIG TGLDIQGGGS
DLIFPHHEYS AAHAESVTGE RRFARHYVHT GMIGWDGHKM
SKSRGNLVLV SQLRAQGVDP SAIRLGLFSG HYREDRFWSN
EVLDEANARL ARWRSATALP EAPDATDVIA RVRQYLADDL
DTPKALAALD GWCTDALSYG GHDTESPRLV ATTVDALLGV DL (SEQ ID
NO: 2)

Figure 2B

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>cysS2: 1242 bp - M. tuberculosis -

atgcagtcgtggtattgccaccggtccggtgttgccgggacgaggcccgagctacgg
ctgtacgacagcgccgaccggcaggtccgtccggtggcgcccgatctaaggccaccatg
tacgtctcggggatcacgccctacgacgccacgcatctgggcatgctgccacctatgtg
acgttcgacctgatccatcggtgtggctggatctcggtcatgaattgcactatgtccag
aacatcaccgacatcgacgatccactattgagcgcgcggtatcgcgacggtgtcgactgg
cgtgaccttggccaagccgaggtcgccctgttctgtgaggacatggcgggcgctgcggggtg
ctaccaccgcaagactacgtggggggccaccgaagcgattgctgaaatggtcgagctcatc
gaaaaaatgtggcgtgcggggcgccctatgtcatagaccgggaaatgggagagtaccag
gacatctacttcgcgctgacgccaccctgcagttcggctacgagtcagggtatgaccgt
gacaccatgctgcggctgtgcgaggaacgtggcgcgcatccgcggcgccccggcaagagc
gacgaactcgacgcgttgttggtggcgggccgcgcggcccggtgagcccagctggccgtcc
ccgttcgggcctggccggccaggctggcatgtcgagtgcgagccatcgcgctcagtcgt
atcgggaagcgccctcgacatccaggcggtggtagcgatctgatcttccgaccacgag
ttcaccgctgcgcacgccgaatgtgtcagcggcgaaacggcgattcgcgcggcactacgtg
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ctggtgtcggcgctgcgtgcgcaggacgttgagccatcggcggttcggctgggttgctc
gccgggacactaccgagccgatcggttctggagccagcaggtgcttgacgagggcgaccgcc
cggctgcaccgttggcgacccgaaccgcacttcccgggtccggccgcagttgacgtt
gtcgctcgggtgcgcccgtacctggccgacgatctcgatacgcccaaagcgattgccgca
ctggatggttgggtcaccgatcggtggagtacggcgggccacgatgccggggcgccgaag
ttggtggcgacggcgatcgatgccctgctcggggtggacctg

Figure 2C

MshC amino acid sequence of *M. tuberculosis* (PMshCMtP1101)

MQSWYCPPVPVLPGRGPQLRLYDSADRQVRPVAPGSKATMYVCGITPYD
ATHLGHAATYVTFDLIHRLWLDLGHELHYVQNITDIDDPLFERADRDGVD
WRDLAQAEVALFCEDMAALRVLPPQDYVGATEAIAEMVELIEKMLACGA
AYVIDREMGEYQDIYFRADATLQFGYESGYDRDTMLRLCEERGDPRRPG
KSDELDALLWRAARPGEPSWPSFPGPRPGWHVECAAIALSRIGSGLDIQG
GGSDLIFPHHEFTAHAECVSGERRFARHYVHAGMIGWDGHKMSKSRGN
LVLVSALRAQDVEPSAVRLGLLAGHYRADRFWSQQVLDEATARLHRWRT
ATALPAGPAAVDVVARVRRYLADDLTPKAIAALDGWVTDAVEYGGHD
AGAPKLVATAIDALLGVDL (SEQ ID NO: 4)

Figure 2D

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MshC amino acid sequence of *Corynebacterium striatum* (AAG03366) (PMshC-Cor.s-GB)

MHAWPDPSVPAVAGTPVPLKLFDTADQRVKEVDTPDANGEVGMVYVCGI
TPYDSTHLGHAATYLTFDLAQRQLLANGHKVHYVQNITDVDDPLFERAER
DGVDWRELGTSQINLFRSDMEILSVIPPCDYIGAMESVDEVIAMVQQLLDA
GAAYELDQGDYASIDATEQFGYESNLDRA TMEEYFAERG GGPDPREGKRD
PLDALVWRGHREGEPAWDSPFGPGRPGWHVECSAIA TNRLGSHFAIQGGG
SDLAFPHHEFSAAHAEAALKVERMAGHYVHAGMIALDGVKMSKSLGNL
V FVHKLSEAGHDPSAIRLAVFAGHYREDRDFSDAILAEAEERLTRWREQL
AGEVSEAEATEVVVDKLRAILADDLNTPEALSLLDGAAGDCNQI IATA LDGL
LGVRI (SEQ ID NO: 5)

Figure 2E

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MshC amino acid sequence of *Streptomyces coelicolor* A3(2) (CAC36366)
(PMshCScGB1101)

MHAWPASEVPALPGQGRDLRIHDTATGGPVTLDPGPVARIYVCGITPYD
ATHMGHAATYNAFDLVQRVWLDTKRQVHYVQNVTDVDDPLLERAVR
DGVDWTALAEQETALFREDMTALRMLPPQHYIGAVEAIPGIVPLVERLR
DAGAAYELEGDVYFSVEADPHFGGVSHLDAATMRLLSAERGGDPDRP
GKKNPLDPMLWMAAREGEPSWDGGTLGRGRPGWHIECVAIALDHLGM
GFDVQGGGSDLAFPHHEMGASHAQALTGEFPMAKAYVHAGMVGLDG
EKMSKSKGNLVFVSQLRREGVDPAAIRLTLLAHHYRSDWEWTDQVLQ
DALARLDRWRAAVSRPDGPPAEALVEEIREALANDLDSPAALAAVDRW
AALQQESGGTDIGAPGVVSRAVDALLGVAL (SEQ ID NO: 6)

Figure 2F

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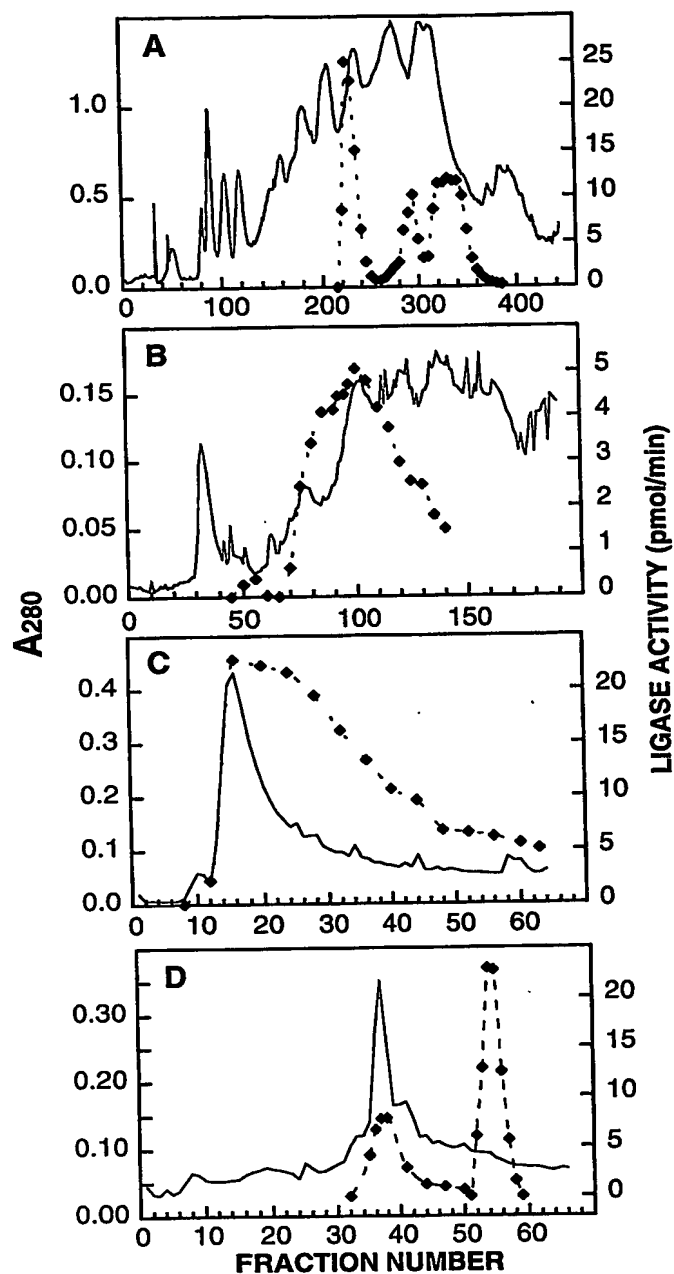


Figure 3

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	1	10	20	30	40	50	61
1. <i>M. smegmatis</i> (1)	MOS	SAP	AL	EV	VP	GR	GH
2. <i>M. tuberculosis</i> (1)	MOS	Y	CE	VE	VL	PG	HC
3. <i>C. striatum</i> (1)	MHA	HE	DE	SV	PA	AG	TP
4. <i>S. coelicolor</i> (1)	MHA	FE	SE	VE	PA	PG	GR
	62	70	80	90	100	110	122
1. <i>M. smegmatis</i> (58)	TV	L	T	E	D	L	V
2. <i>M. tuberculosis</i> (58)	TV	T	E	D	L	V	E
3. <i>C. striatum</i> (62)	TV	T	E	D	L	V	E
4. <i>S. coelicolor</i> (58)	TV	T	E	D	L	V	E
	123	130	140	150	160	170	183
1. <i>M. smegmatis</i> (119)	R	V	L	P	H	D	V
2. <i>M. tuberculosis</i> (119)	R	V	L	P	H	D	V
3. <i>C. striatum</i> (123)	R	V	L	P	H	D	V
4. <i>S. coelicolor</i> (119)	R	V	L	P	H	D	V
	184	190	200	210	220	230	244
1. <i>M. smegmatis</i> (178)	R	T	M	I	T	L	E
2. <i>M. tuberculosis</i> (180)	R	T	M	I	T	L	E
3. <i>C. striatum</i> (179)	R	T	M	I	T	L	E
4. <i>S. coelicolor</i> (174)	R	T	M	I	T	L	E
	245	250	260	270	280	290	305
1. <i>M. smegmatis</i> (238)	R	I	G	S	H	F	A
2. <i>M. tuberculosis</i> (240)	R	I	G	S	H	F	A
3. <i>C. striatum</i> (239)	R	I	G	S	H	F	A
4. <i>S. coelicolor</i> (235)	R	I	G	S	H	F	A
	306	320	330	340	350	366	
1. <i>M. smegmatis</i> (299)	I	V	S	O	L	R	E
2. <i>M. tuberculosis</i> (301)	I	V	S	O	L	R	E
3. <i>C. striatum</i> (300)	I	V	S	O	L	R	E
4. <i>S. coelicolor</i> (296)	I	V	S	O	L	R	E
	367	380	390	400	410	420	
1. <i>M. smegmatis</i> (359)	I	A	R	V	R	O	L
2. <i>M. tuberculosis</i> (361)	I	A	R	V	R	O	L
3. <i>C. striatum</i> (361)	I	A	R	V	R	O	L
4. <i>S. coelicolor</i> (356)	I	A	R	V	R	O	L

Figure 4

10/30

1. MshC M. tuberc. (1)	1	10	20	30	40	50	66
2. CysS M. tuberc. (1)	1	10	20	30	40	50	66
3. CysS E. coli (1)	1	10	20	30	40	50	66
1. MshC M. tuberc. (64)	67	80	90	100	110	120	132
2. CysS M. tuberc. (54)	67	80	90	100	110	120	132
3. CysS E. coli (49)	67	80	90	100	110	120	132
1. MshC M. tuberc. (130)	133	140	150	160	170	180	198
2. CysS M. tuberc. (120)	133	140	150	160	170	180	198
3. CysS E. coli (115)	133	140	150	160	170	180	198
1. MshC M. tuberc. (196)	199	210	220	230	240	250	264
2. CysS M. tuberc. (177)	199	210	220	230	240	250	264
3. CysS E. coli (175)	199	210	220	230	240	250	264
1. MshC M. tuberc. (262)	265	270	280	290	300	310	330
2. CysS M. tuberc. (240)	265	270	280	290	300	310	330
3. CysS E. coli (238)	265	270	280	290	300	310	330
1. MshC M. tuberc. (328)	331	340	350	360	370	380	396
2. CysS M. tuberc. (303)	331	340	350	360	370	380	396
3. CysS E. coli (302)	331	340	350	360	370	380	396
1. MshC M. tuberc. (390)	397	410	420	430	440	450	462
2. CysS M. tuberc. (369)	397	410	420	430	440	450	462
3. CysS E. coli (368)	397	410	420	430	440	450	462
1. MshC M. tuberc. (434)	463	470	480	498			
2. CysS M. tuberc. (431)	463	470	480	498			
3. CysS E. coli (431)	463	470	480	498			

Figure 5

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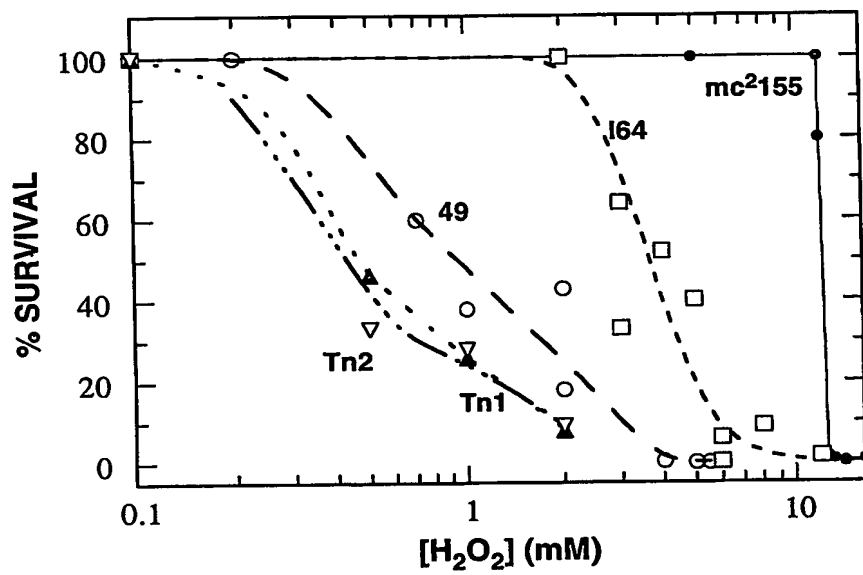
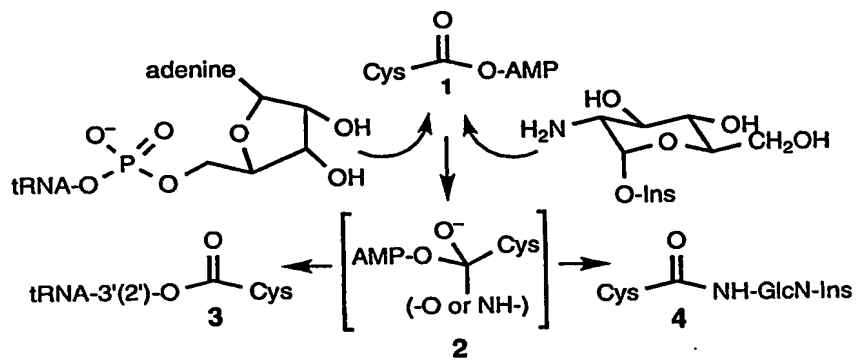


Figure 6

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**Figure 7**

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		1		50
<i>M. tuberculosis</i>	(1)	-----VTALDWRSALTAD	EQRSVRALVTATTAVDGVAPVGEQV-	
<i>M. smegmatis</i>	(1)	-----VTSTEWRTGLTGACQAEIRALID	AATHDGVAPVGDQV-	
<i>M. leprae</i>	(1)	-----MVLNRRFALSAD	EQRLVREIISAATEFDEVPVGEQV-	
<i>S. coelicolor</i>	(1)	MTSDDTVRPGRP	RSIETLAEITPEQTD	AVLALLTEAARTDGOHAVSEQGR
<i>C. diphtheriae</i>	(1)	-----MIETSLASAS	AALRDRVDEILAAATREDGCAPLSE	SFL
		51		100
<i>M. tuberculosis</i>	(39)	--LRELQOORTEHLLVAGSRPGCE	IIIGYLNLSPPRCAGGAMAELVVHPQS	
<i>M. smegmatis</i>	(39)	--LRELGRDRTRHLLTTDD---	DRVVGYLNLAPEGDDPAMAELVVHPQA	
<i>M. leprae</i>	(38)	--LRELGYDRTEHLLVTD	SRFYAIIIGYLNLSPPRDAGVAMAELVVHPR	
<i>S. coelicolor</i>	(51)	LQLRGPA	REGVVHLLLTLD--GGELVGYAOLEG	TDVVEPPAAELVVHPSH
<i>C. diphtheriae</i>	(39)	NGLRR-ADDGHVHSCVMDS--	HDQVVG---VAARDGDS---AEVVVDPAF	
			-----pfam00583-	
		101		150
<i>M. tuberculosis</i>	(87)	RRRGIGTAMARAALAKTAGRNQFWAHG	TLDPARATASALGLVGVRELITQM	
<i>M. smegmatis</i>	(84)	RRRGIGAAMARTALAE	GGPGARIWAHCNIAAAQAMASSRLV	VVRELLQM
<i>M. leprae</i>	(86)	RRRGVGAAMVRAALAKTGGRNR	FWAHGTLASARATASVLGLVPVREL	VQM
<i>S. coelicolor</i>	(99)	RGCGHGRALGSALLAASGKRLRI	WAHGHSAARHLAQVLGLSLFREL	RQL
<i>C. diphtheriae</i>	(80)	RRQGYGSFLIRHVVSQGVKN--	VWAHGDGAGAKAVAKALQLEQTR	OLLVM

		151		200
<i>M. tuberculosis</i>	(137)	RRPL-R--DIPEFTIPD--	GVVI---RTYAGTSD--DAELLRVNNAAFAG	
<i>M. smegmatis</i>	(134)	RRPL-T--DLP-P--VPDTPGVRI---	ATYAGPGD--DAELLRVNNAAFSW	
<i>M. leprae</i>	(136)	QRSL-R--TIPDPMPDQLGVWV---	RTYVGTVD--DAELLRVNNAAFAG	
<i>S. coelicolor</i>	(149)	RRPL-TGLDLPEPRIPE--	GVSV---RTFVPGQD--DAAWLAVNNAAF	FAH
<i>C. diphtheriae</i>	(128)	AVEGDRLVESAQLQVPS--	GFRVLALNEAVESIPDIEQQLRVNNEAF	FEW

		201		250
<i>M. tuberculosis</i>	(177)	HPEQGGWTA	VQLAERRCEAWF--DPDGLILAFGDS	SPRERPGRLILGFHWTKV
<i>M. smegmatis</i>	(174)	HPEQGGWTEHEIDER	NEGWF--DPEGLFOAFD---EQTGS	LLGFHWTKI
<i>M. leprae</i>	(178)	HPEQGGWTATQLAERR	SEPWF--DPAGLFLAFGDSSSNQ	PGKILGFHWTKV
<i>S. coelicolor</i>	(191)	HPEQGSILTQ	RDLDKAE	PWF--DPAGFFLA-----ERDGE
<i>C. diphtheriae</i>	(176)	HPEQGGWDSARLAQ	ARDTQNERESDVLF	LID-----TAKRTVAGFHWTKR

		251		300
<i>M. tuberculosis</i>	(226)	HPD--HPGLGEVYVLGVDPAAQRR	GLGQMLTSGIVSLARRLGGRKTLD	P
<i>M. smegmatis</i>	(219)	HD---ASLGEVYVLGVDP	QAQGRGLGYTLTLIGLHHLAEKLAG	---P
<i>M. leprae</i>	(227)	HAA--HPGLGEVYVLGVDP	SAQGRGLGQMLTSGIASLAQR	LVG---P
<i>S. coelicolor</i>	(234)	HA---EERLGEVYVLGIRE	DTQGGGLGKALTITGLRHLEGO	--G-----
<i>C. diphtheriae</i>	(221)	HGDLAEGADGEVYVLG	LSAYRRRGLGDLIRMGLHHL	EYEHAR-----
			-----pfam00583-	
		301		343
<i>M. tuberculosis</i>	(274)	AVEPAVLLYVESDNVAAV	RTYQSLGFTTYSVDTAYALAGTDN-	
<i>M. smegmatis</i>	(260)	--EPTVLLYVEADNSAAVNTY	RKLGFEVFSVDAAYAAN----	
<i>M. leprae</i>	(270)	SAEPTVMLYVESDNVAAARTY	ERLGF	TYSVDTAYALARIDD-
<i>S. coelicolor</i>	(273)	--LPTAMLYVDADNKAAV	VERLGFVTHETDLMV	RTET----
<i>C. diphtheriae</i>	(265)	--R--VILYVEGDNESARRA	YDALGFHVESHVTS	SPQSSS--

Figure 8

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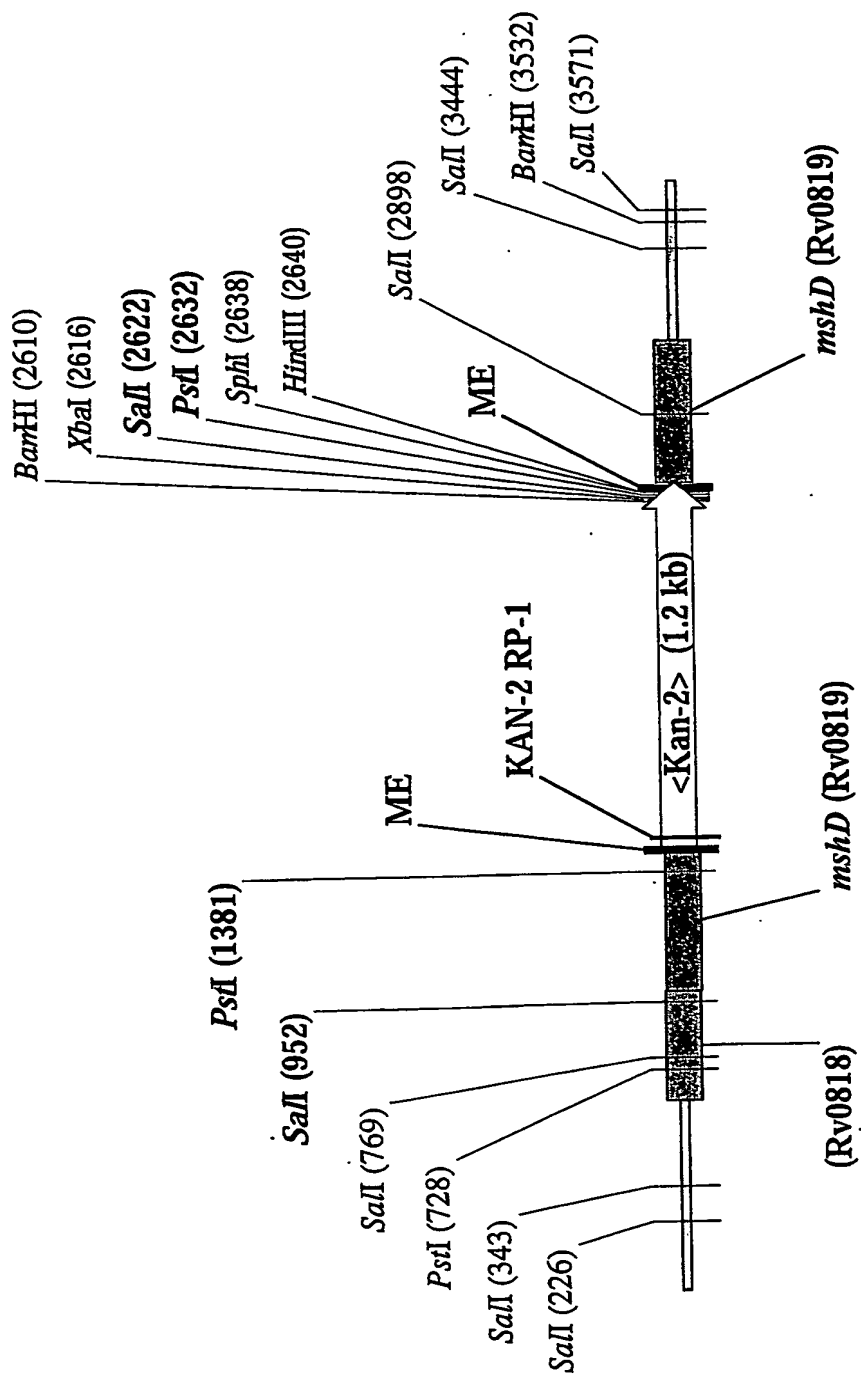


Figure 9

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MshD amino acid sequence of *M. tuberculosis* (CAA17625.1) (Rv0819)

MTALDWRSALTAEQRSVRALVTATTAVDGVAPVGEQVLRELGQQRT
EHLVAGSRPGGPPIIGYLNLSPPRGAGGAMAELVVHPQSRRRGIGTAMA
RAALAKTAGRNQFWAHGTLDPARATASALGLVGVRELIQMRRPLRDIP
EPTIPDGVVIRTYAGTSDDAELLRVNNAAFAGHPEQGGWTAVQLAERR
GEAWFDPDGLILAFGDSPRERPGRLLGFHWTKVHPDHPGLGEVYVLGV
DPAAQRRGLGQMLTSIGIVSLARRLGGRKTLDPAVEPAVLLYVESDNVA
AVRTYQSLGFTTYSVDTAYALAGTDN (SEQ ID NO: 14)

Figure 10A

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MshD amino acid sequence of *M. smegmatis* (PMshDMs-Tr)

VTSTEWRTGL TGAQQAEIRA LIDAATTHDG VAPVGDQVLR
ELGRDRTRHL LTTDDDRVVG YLNLAPAEGD DPAMAELVVH
PQARRRGIGA AMARTALAEG GPGARIWAHG NIAAAQAMAS
SLRLVVVREL LQMRRPLTDL PPVPDTPGVR IATYAGPGDD
AEILRVNNAA FSWHPEQGGW TEHEIDERN EGWFDPEGLF
QAFDEQTGSL LGFHWTKIHD ASLGEVYVVG VDPQAQGRGL
GYTLTLIGLH HLAEKLAGPE PTVLLYVEAD NSAAVNTYRK
LGFEVFSVDA AYAAN (SEQ ID NO: 15)

Figure 10B

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MshD amino acid sequence of *M. leprae* (ML2193)

MVLNWRFALESADEQRLVREIISAATEFDEVSPVGEQVLRELGYDRTEHL
LVTDSRPYAPIIGYLNLSRPDAGVAMAELVVHPRERRRGVGAAMVRA
ALAKTGGRNRFWAHGTLASARATASVLGLVPVREL VQMQRSLRTIPDP
MVPDQLGVWVRTYVGTVDDAELLRVNNAAFAGHPEQGGWTATQLAE
RRSEPWFDPAFLAFLAGDSSSNQPGKLLGFHWTKVHAAHPGLGEVYVL
GVDPSAQGRGLGQMLTSIGIASLAQRLVGPSAEPTVMLYVESDNVAAA
RTYERLGFTTYSVDTAYALARIDD (SEQ ID NO: 16)

Figure 10C

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MshD amino acid sequence of *Streptomyces coelicolor* (SCD84.18c, SCO4151)

MTSDDTVRPGRPRSIETLAELTPEQTDVLAALLTEAARTDGQHAVSEQG
RLQLRGPAAREGVVHLLLTLDGGELVGYAQLEGTDPEPPAAELVVHPS
HRGQGHGRALGSALLAASGKRLRIWAHGGHSAARHLAQVLGLSLFREL
RQLRRPLTGLDLPEPRLPEGVSVRTFVPGQDDAAWLAVNAAFAHHPE
QGSLTQRDLDDRKAEPWFDPAGFFLAERDGELIGFHWTKVHAEERLGE
VYVLGIRPDTQGGGLGKALTTIGLRHLEGQGLPTAMLYVDADNKAAVA
VYERLGFVTHETDLMYRTET (SEQ ID NO: 17)

Figure 10D

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MshD amino acid sequence of *Corynebacterium diphtheriae* (PMshDCd-Tr)

MIETSLASAS AALRDRVDEI LAAATREDGC APLSESFLNG
LRRADDGHVH SCVMDSHDQV VGVAARDGDS AEVVVDPAFR
RQGYGSFLIR HVVSQGVKNV WAHGDGAGAK AVAKALQLEQ
TRQLLVMAVE GDRLVESAQL QVPSGFRVLA LNEAYESIPD
IEQQWLRVNN EAFEWHPEQG GWDSARLAQA RDTQWFRES
VLFLIDTAKR TVAGFHWTKR HGDLAEGADG EVYVVGLGSA
YRRRGLGDLL IRMGLHHLEY EHARRVILYV EGDNESARRA
YDALGFHVVE SHVTYSPQSS S (SEQ ID NO: 18)

Figure 10E

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Nucleic acid sequence *mshD* *M. smegmatis*, including stop codon

GTGACCTCCACCGAGTGGCGCACCGGGCTCACGGGTGCCCAGCAGG
CAGAGATTCGCGCGCTGATCGACGCGGCCACCACGCACGACGGTGT
CGCGCCGGTCGGTGACCAAGTGCTGCGGGAAC TGGGACGCGACCGC
ACCGGGCACCTGCTGACCACCGACGACGACCGCGTGGTCGGATACCT
CAACCTCGCGCCTGCCGAGGGGGACGATCCGGCGATGGCCGAAC TC
GTCGTGCATCCGCAGGCCCGCCGGCGCGGTATCGGTGCGGCCATGGC
GCGCACCGCGCTGGCAGAGGGCGGGGCCGGGCGCCCGTATCTGGGCG
CACGGCAACATCGCCGCCGCCAGGCGATGGCGTCATCGCTTCGCCT
GGTGGTGGTGC GTGAGCTGCTGCAGATGCGCCGCCCCCTGACCGATC
TGCCGCCGGTGCCGGACACCCCCGGCGTGCGCATCGCGACCTACGCC
GGCCCCGGCGACGACGCCGAGATCCTGCGGGTCAACAACGCCGCGT
TCTCGTGGCACCCCGAGCAGGGCGTGA (SEQ ID NO: 48)

Figure 10F

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MshA-Msmeg 1-----VRLATDLET PRRVAVLSVHTSPLAQPGTGDA 1-
MshA-Mtub 1MAGVRHDDGSLIAQRRPVRGEGATRSRGPSPGSPNENNSAADDPRRVALLAVHTSPLAQPGTGDA
SpsA-Anab 1-----MFQNKKHRIALISVSGDPAVEIGQEEA
PimB-Mtub 1-----VCGVRVAIVAESFLPQVN-----
          *-BOX I--|
MshA-Msmeg 32GGMNVYVLQ TALQLARRGV EVEVFTRATSSADAPVVPVAPGVLVRNVVAGPFEGLDKNDLPTQLC
MshA-Mtub 66GGMNVYMLQSALHLARRGIEVEVFTRATASADFPVVRVAPGVLVRNVVAGPFEGLDKNDLPTQLC
SpsA-Anab 28GGQNVYVREVGYALAEQGWQVDMETTRISPDQAEIVQHS PNCRTIRLQAGPVEFGRDHVFDYLP
PimB-Mtub 19-GVSN SVVKVLEHLRRTCHEALVTAPDTPPGEDRAERLHDGVRVHRVPSRMFPKVT--TLELGVP

MshA-Msmeg 97AFTAGVLR AEATHEPGY-YDVVHSHY-WLSGQVGWLARDRWAVPLVHTAHTLA AVKNAALAAAGDA
MshA-Mtub 131AFAAGVLR AEAVHEPGY-YD IVHSHY-WLSGQVGWLARDRWAVPLVHTAHTLA AVKNAALADGDG
SpsA-Anab 93EFVAEFQRFQK--RQGYNYQLIBTNY-WLSSWVGMLKKQQLVVLVHTYHSLGAIKYQTIA--DI
PimB-Mtub 81TFR--MLRALR----GFDPDVVHLASPA LLGYGGLHAARRLG VPTVAVYQTDVPFGASSYG---I
          G242↓ ↓D244
MshA-Msmeg 160PEPPLRAVGEQQQVDEADRLIVNTEVEAQQLVSLHNADRSRIDVVHHPGVLDLDFETPGSRDAARAV
MshA-Mtub 194PEPPLRTVGEQQVDEADRLIVNTDDEARQVISLHGADPARIDVVHHPGVLDLDFETPGDRRAARAA
SpsA-Anab 153PAIANQRLAIEKACLESVDTVVATSPQEQQHMRALVSKKGRIEMI PCGTDINNEGNI EKSAAREK
PimB-Mtub 137PMTARAAWAWFRHLHRLADRTLAPSTATMESLIAQGIP--RVHRWARGVDVQREAF SARNEVLRR
          R273↓ ↓K278
MshA-Msmeg 225EGLPTDOKIVAFVVGRIQPLKAPDILLRAAAK-----LPGVRVLIAGG--PSGSGLAOPDTLVRLA
MshA-Mtub 259LGLEVDERVVAFVVGRIQPLKAPDIVLRAAAK-----LPGVRIIVAGG--PSGSGLASPDGLVRLA
SpsA-Anab 218LGIEPDAMV FVYVGRFDPKGIETLVRAVAQSR LRGEANLQLVIGGSRFGQSDGRERDRIANIV
PimB-Mtub 200RWS E DGKPIVGFVGR LAPEKHVURLTGLAAS-----GAVRLVIVG-----DGIDFAR
          E354↓-----BOX II-----|
MshA-Msmeg 283DELGISDRVTFLPPQSREQLVNVYRAADLVAVPSYSESFGLVAVEAQACGTPVVA AVVGGLPVAV
MshA-Mtub 317DELGISARVTFLPPQSH TDLATLFRAADLVAVPSYSESFGLVAVEAQACGTPVVA AVVGGLPVAV
SpsA-Anab 283AELELNDCTTFAGRLDHEILPYYIAADVCVVP SHYEPFGLVATEAMASKTPVIASNVGGLQFTV
PimB-Mtub 247LQSAMPT-AVFTGARYGKELAEAYASMDV FVHSGEHETFCQVVOEALASGLPVIA PDAGGPRDLI

MshA-Msmeg 348ADGVSGALVD-GHDIGDWADTI SEVLDREPA----ALSRASAEHAAQFSWAHTVDALLASYSRAM
MshA-Mtub 382RDGITGTLVS-GHEVGQWADAIDHLLRLCAGPRGRVMSRAAARHAATFSWENTTDALLASYRRAI
SpsA-Anab 348VPEVTGLLAP-PQDESAFATAIDRILANPTWR-DQLGTAAARQVETTFSWAGVASOLSQLYTHLL
PimB-Mtub 311TPHRTGLLL PVGEFEHRLPDVAH L VHERQR-----YALAA RRSVLGRSWPVVCD ELLGHYEAVR

MshA-Msmeg 408SDYRARHPRPA-----ARRSGRRFSMRRGVRT
MshA-Mtub 446GEYNAERORRGGEVISDLVAVGKPRHWTFRRGVGA
SpsA-Anab 411TONAPEKKEKE-----AVAA-----
PimB-Mtub 371GRRTTQAA-----

```

Figure 11

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MshA amino acid sequence of *M. smegmatis* (PMshAMs-Tr)

VRLATDLETP RRVAVLSVHT SPLAQPGTGD AGGMNVYVLQ
TALQLARRGV EVEVFTRATS SADAPVVPVA PGVLVRNVVA
GPFEGLDKND LPTQLCAFTA GVLRAEATHE PGYYDVVHSH
YWLSGQVGWL ARDRWAVPLV HTAHTLAAVK NAALAAGDAP
EPPLRAVGEQ QVVDEADR LI VNTEVEAQQL VSLHNADRSR
IDVVHPGV DL DVFTPGSRDA ARAVFGLPTD QKIVAFVGRI
QPLKAPDILL RAAAKLPGVR VLIAGGPSGS GLAQPD TLVR
LADELGISDR VTFLPPQSRE QLVNVYRAAD LVAVPSYSES
FGLVAVEAQA CGTPVVAAAV GGLPVAVADG VSGALVDGHD
IGDWADTISE VLDREPAALS RASAEHAAQF SWAHTVDALL
ASYSRAMSDY RARHPRPAAR RSGRRFSMRR GVRT (SEQ ID NO: 19)

Figure 12A

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MshA amino acid sequence of *M. tuberculosis* (PMshAMtG1002)

MAGVRHDDGS GLIAQRRPVR GEGATRSRGP SGPSNRNVSA
ADDP RR VALL AVHTSPLAQP GTGDAGGMNV YMLQSALHLA
RRGIEVEIFT RATASADPPV VRVAPGVLVR NVVAGPFEG
L DKYDLPTQLC AFAAGVLRAE AVHEPGYYDI VHSHYWLSGQ
VGWLARDRWA VPLVHTAHTL AAVKNAALAD GDGPEPPLRT
VGEQQVVDEA DRLIVNTDDE ARQVISLHGA DPARIDVVHP
GVDLDVFRPG DRRAARAALG LPVDERVVA F VGRIQPLKAP
DIVLRAAAKL PGVRIIVAGG PSGSGLASPD GLVRLADELG
ISARVTFLPP QSHTDLATLF RAADLVAVPS YSESFGLVAV
EAQACGTPVV AA AVGGLPVA VRDGITGTLV SGHEVGQWAD
AIDHLLRLCA GPRGRVMSRA AARHAATFSW ENT TDALLAS
YRRAIGEYNA ERQRRGGEVI SDLVAVGKPR HWTPRRGVGA (SEQ ID
NO: 20)

Figure 12B

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Nucleic acid sequence *mshA* *M. smegmatis*, including stop codon

GTGCGTCTAGCGACAGACCT
CGAGACCCCCCGCCGCGTGGCGGTGTTGTCGGTACACACCTCTCCGC
TGGCGCAGCCGGGCACCGGCGACGCGGGCGGCATGAACGTCTACGT
GTTGCAGACCGCGCTGCAACTGGCCCCGGCGTGGCGTCGAGGTCGAG
GTCTTCACCAGGGCCACGTCGTCGGCCGATGCGCCGGTTCGTGCCTGT
GGCGCCCCGGTGTGCTGGTGC GCAACGTCGTGGCCGGCCCCGTTCTGAAG
GCCTCGACAAGAACGATCTGCCACGCAGCTGTGCGCGTTTACC GCG
GGTGTGCTGCGCGCCGAGGCGACCCACGAGCCCCGGCTACTACGACG
TCGTGCATTTCGCACTACTGGCTGTCCGGCCAGGTCGGGTGGCTGGCG
CGCGACCGCTGGGCCGTGCCGCTGGTGCACACCGCGCACACGCTGG
CCGCGGTCAAGAACGCCGCACTCGCCGCGGGCGACGCACCCGAGCC
GCCGCTGCGCGCGGTGGGCGAACAACAGGTGGTCGACGAGGCCGAC
CGCCTCATCGTGAACACCGAAGTCGAAGCGCAGCAACTGGTCTCGTT
GCACAATGCCGACCGCTCACGCATCGACGTCGTGCACCCCGGCGTCG
ATCTCGACGTGTTTACCCCCGGTTCGCGCGACGCGGCGCGCGCGGTG
TTCGGGCTTCCCACCGACCAAGAATCGTGGCGTTCGTGGGCCGCAT
CCAGCCGCTCAAGGCCCGGACATCCTGCTGCGTGCCGCGGGCGAAAC
TGCCCGGCGTGCGCGTGCTGATCGCCGGTGGACCCTCCGGATCGGGA
CTTGCCCAACCGGACACGCTGGTTCGGCTCGCCGACGAAC TGGGTAT
CAGTGACCGGGTGACGTTCTCCCGCCGACAGCCGCGAACA ACTG
GTCAACGTGTACCGGGCGGCGCGATCTGGTCGCGGTGCCGAGCTACTC
CGAGTCGTTTCGGCCTGGTTCGCCGTCGAGGCGCAGGCGTGCGGCACGC
CCGTCGTCGCCGCGGCGGCTCGGCGGACTGCCGGTCGCGGTGGCCGAC
GGCGTCAGCGGGGCACTCGTCGACGGCCACGACATCGGCGACTGGG
CCGACACCATCAGCGAGGTGCTCGACCGCGAGCCCGCCGCGCTGAG
CCGCGCCTCCGCCGAACACGCCGCTCAGTTCTCGTGGGCGCACACCG
TCGACGCGCTGCTCGCCAGCTACAGCCGGGGCCAT
GAGTGACTACCGGGCCCGTCATCCCAGACCCGCCGCGCGGCGTTCCG
GACGCCGTTCTCGATGCGCAGGGGAGTACGCACGTGA (SEQ ID NO:
49)

Figure 12C

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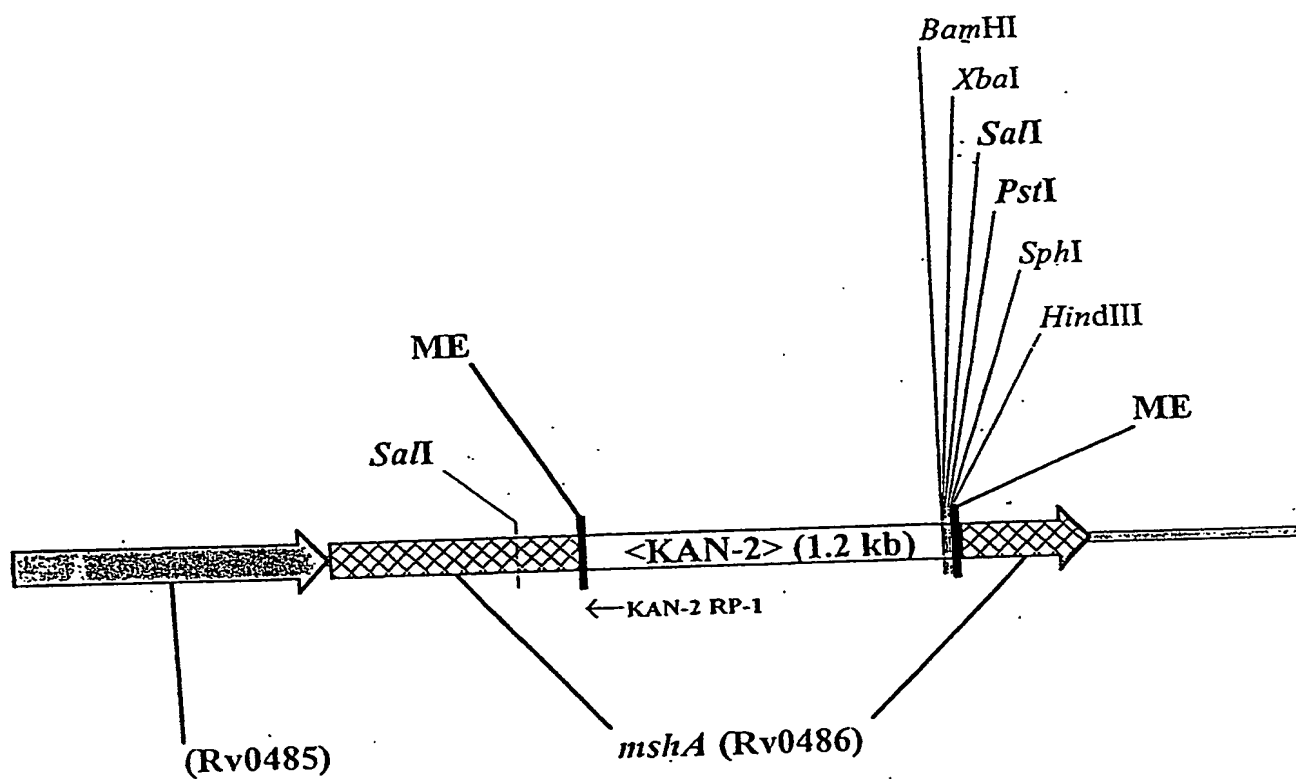
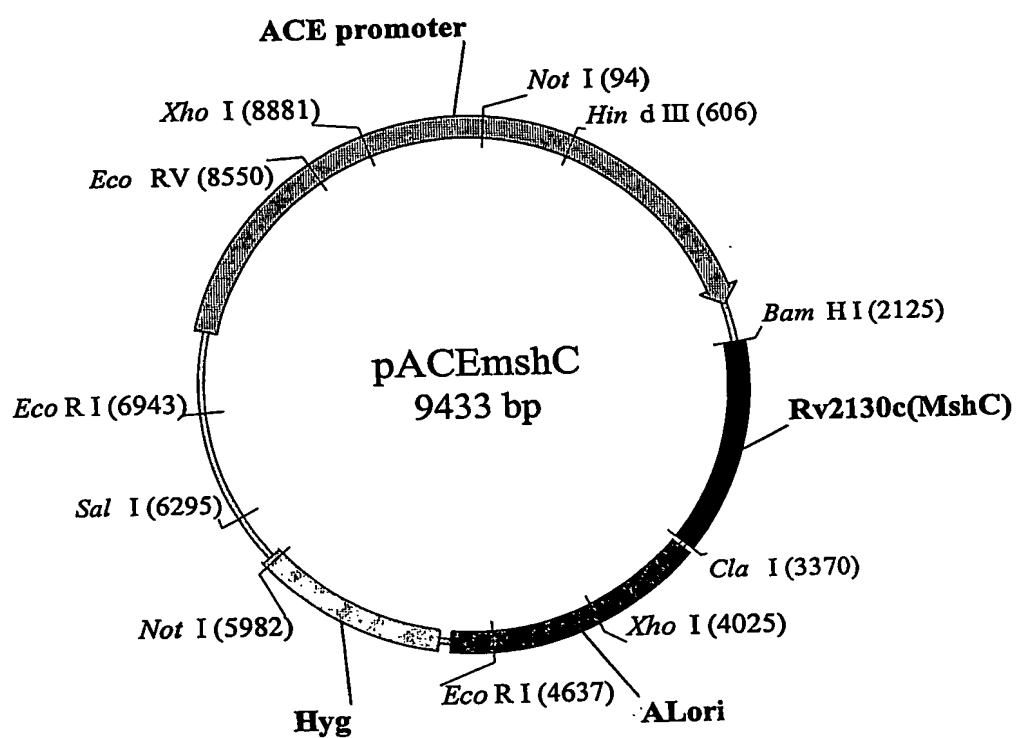
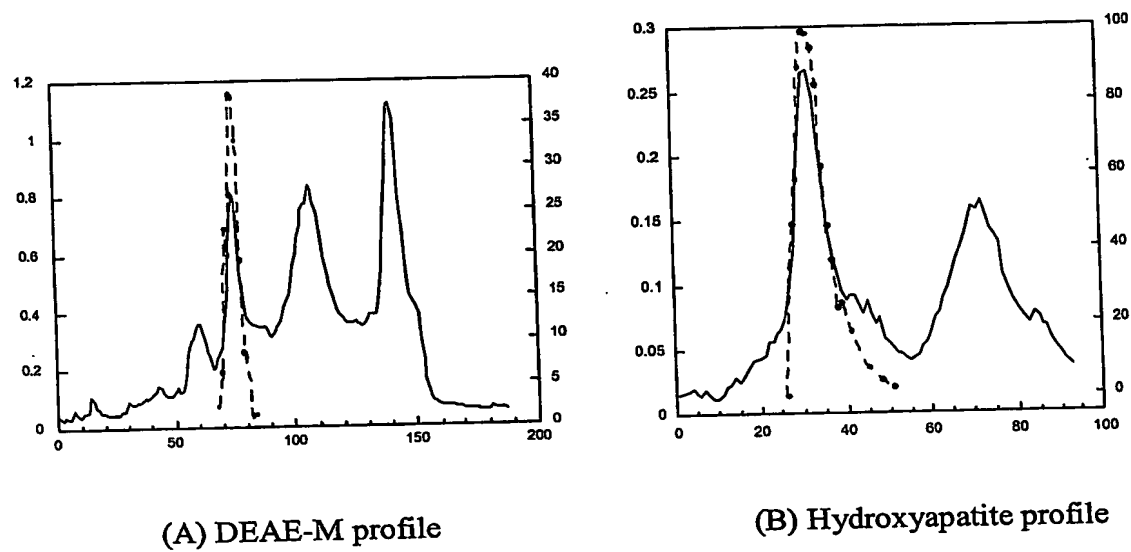


Figure 13

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**Figure 14**

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**Figure 15**

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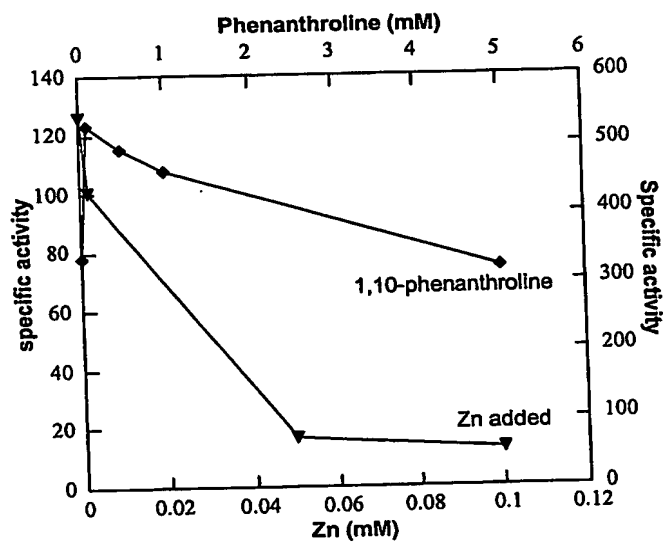


Figure 16

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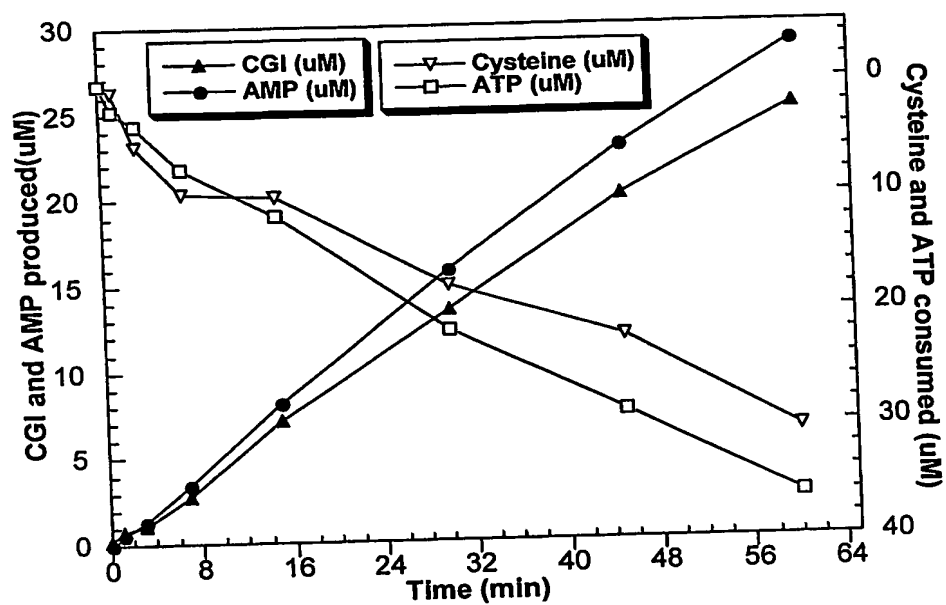


Figure 17

30/30

(a) First Half of Rossman fold:

M. smeg MshC (40) --MYVCGITPYDATHLGHAAATYLTFDL (64)
M. lepr Mshc (11) ATMYVCGITPYDATHLGHAAATYLAFDL (37)
S. coel. MshC (40) --IYVCGITPYDATHMGMHAATYNAFDL (64)
C. strt. MshC (44) --MYVCGITPYDSTHLGHAAATYLTFDL (68)
T. bifi. MshC (40) --MYVCGITPYDAAHLGHAAATYLTFDL (64)
M. tubr Cyss (30) --IYLCGATVQGLPHIGHVRSGVAFDI (54)
E. coli Cyss (25) --MYVCGITVYDLCHIGHGRTEFVAFDV (49)

(b) Second half of Rossman Fold:

M. smeg MshC (218) SPFGGRPRGWHVECSAIALTRIGTGLDIQGGGSDLIFFHHHEYSAAHAE SVT
M. lepr MshC (190) SPFGGRPRGWHVECAIALSRIGIGLDIQGGGSDLIFFHHEFTAAHAE CVR
S. coel. MshC (215) GTLGRGRPGWHIECVAILDLHGMGFDVQGGGSDLAFFHHHEMGASHAQALT
C. strt. MshC (219) SPFGGRPRGWHVECSAIAIATNRLGSHFAIQGGGSDLAFFHHHEFSAAHAEAL
T. bifi. MshC (198) TPLGRGRPGWHVECSAISVHEIGMGFDLNGGGDDLIFPHHEMGAAEACCAT
M. tubr Cyss (214) TPWGRGRPGWHLECSAMARSYLGPFDIHC GGMDLVFPHHENETIAQSRAAG
E. coli Cyss (196) SPWGAGRPGWHIECSAMNCKQLGNHFDIHGGGSDLMFPHHENEETIAQSTCAH

M. smeg MshC GERREARHYVHTGMIGWDGHKMSKS (293)
M. lepr Mshc GERREARHYVHAGMIGWDEHKMSKS (265)
S. coel. MshC GEFPMAKAYVHAGMVGLDGEKMSKS (290)
C. strt. MshC KVERMAGHYVHAGMIALDGVKMSKS (294)
T. bifi. MshC GSRPQARHYLHVAMVGLDGEKMSKS (289)
M. tubr Cyss DG--FARYWLHNGWVTMGGEKMSKS (271)
E. coli Cyss DGQ-YVNYWMHSGVMVMDREKMSKS (270)

Figure 18

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